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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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## Entry information

| | |
|---|---|
| Entry name | **SPB7_HUMAN** |
| Primary accession number | **O75635** |
| Secondary accession numbers | None |
| Entered in Swiss-Prot in | Release 41, February 2003 |
| Sequence was last modified in | Release 41, February 2003 |
| Annotations were last modified in | Release 41, February 2003 |

## Name and origin of the protein

| | |
|---|---|
| Protein name | **Megsin** |
| Synonyms | **TP55**<br>**Serpin B7** |
| Gene name | **SERPINB7** |
| From | Homo sapiens (Human) [TaxID: 9606] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |

## References

[1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=97326116; PubMed=9182567; [NCBI, ExPASy, EBI, Israel, Japan]
Tsujimoto M., Tsuruoka N., Ishida N., Kurihara T., Iwasa F., Yamashiro K., Rogi T., Kodama S., Katsuragi N., Adachi M., Katayama T., Nakao M., Yamaichi K., Hashino J., Haruyama M., Miura K., Nakanishi T., Nakazato H., Teramura M., Mizoguchi H., Yamaguchi N.;
"Purification, cDNA cloning, and characterization of a new serpin with megakaryocyte maturation activity.";
J. Biol. Chem. 272:15373-15380(1997).

[2] SEQUENCE FROM NUCLEIC ACID.
**TISSUE**=Mesangial cells;
MEDLINE=98376492; PubMed=9710452; [NCBI, ExPASy, EBI, Israel, Japan]
Miyata T., Nangaku M., Suzuki D., Inagi R., Uragami K., Sakai H., Okubo K., Kurokawa K.;
"A mesangium-predominant gene, megsin, is a new serpin upregulated in IgA nephropathy.";
J. Clin. Invest. 102:828-836(1998).

## Comments

- ***FUNCTION***: Might function as an inhibitor of Lys-specific proteases. Might influence the maturation of megakaryocytes via its action as a serpin.

- ***SUBCELLULAR LOCATION***: Cytoplasmic *(By similarity)*.
- ***TISSUE SPECIFICITY***: Predominantly expressed in mesangial cells.
- ***SIMILARITY***: Belongs to the serpin family. Ov-serpin subfamily.

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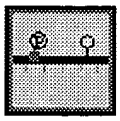
## Cross-references

| | |
|---|---|
| EMBL | D88575; BAA31232.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>AF027866; AAC64506.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] |
| HSSP | P05619; 1HLE. [HSSP ENTRY / PDB] |
| Genew | HGNC:13902; SERPINB7. |
| CleanEx | HGNC:13902; SERPINB7. |
| MIM | 603357 [NCBI / EBI]. |
| GeneCards | SERPINB7. |
| GeneLynx | SERPINB7; Homo sapiens. |
| GO | GO:0004868;Molecular function: serpin *(traceable author statement)*. |
| SOURCE | SERPINB7; Homo sapiens. |
| Ensembl | O75635; Homo sapiens. [Entry / Contig view] |
| InterPro | IPR000215; Serpin.<br>Graphical view of domain structure. |
| Pfam | PF00079; serpin; 1. |
| SMART | SM00093; SERPIN; 1. |
| PROSITE | PS00284; SERPIN; 1. |
| ProDom | [Domain structure / List of seq. sharing at least 1 domain] |
| HOVERGEN | [Family / Alignment / Tree] |
| BLOCKS | O75635. |
| ProtoNet | O75635. |
| ProtoMap | O75635. |
| PRESAGE | O75635. |
| DIP | O75635. |
| ModBase | O75635. |
| SWISS-2DPAGE | Get region on 2D PAGE. |

## Keywords

**Serpin**; **Serine protease inhibitor**.

## Features

 Feature table viewer

| Key | From | To | Length | Description |
|---|---|---|---|---|
| ACT_SITE | 347 | 348 | | REACTIVE BOND (*BY SIMILARITY*). |

## Sequence information

Length: **380 AA** Molecular weight: **42904 Da** CRC64: **9A2CDB6C63CFF605** [This is a checksum on the sequence]

```
        10          20          30          40          50          60
         |           |           |           |           |           |
MASLAAANAE FCFNLFREMD DNQGNGNVFF SSLSLFAALA LVRLGAQDDS LSQIDKLLHV

        70          80          90         100         110         120
         |           |           |           |           |           |
NTASGYGNSS NSQSGLQSQL KRVFSDINAS HKDYDLSIVN GLFAEKVYGF HKDYIECAEK

       130         140         150         160         170         180
         |           |           |           |           |           |
LYDAKVERVD FTNHLEDTRR NINKWVENET HGKIKNVIGE GGISSSAVMV LVNAVYFKGK

       190         200         210         220         230         240
         |           |           |           |           |           |
WQSAFTKSET INCHFKSPKC SGKAVAMMHQ ERKFNLSVIE DPSMKILELR YNGGINMYVL

       250         260         270         280         290         300
         |           |           |           |           |           |
LPENDLSEIE NKLTFQNLME WTNPRRMTSK YVEVFFPQFK IEKNYEMKQY LRALGLKDIF

       310         320         330         340         350         360
         |           |           |           |           |           |
DESKADLSGI ASGGRLYISR MMHKSYIEVT EEGTEATAAT GSNIVEKQLP QSTLFRADHP

       370         380
         |           |
FLFVIRKDDI ILFSGKVSCP
```

O75635 in FASTA format

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ScanProsite, MotifScan

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